

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/574,819**

DATE: 07/31/2001  
 TIME: 14:00:36

Input Set : N:\Crf3\RULE60\09574819.txt  
 Output Set: N:\CRF3\07312001\I574819.raw

**SEQUENCE LISTING**

5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: Luyten, Frank P.  
 8 Moos, Jr., Malcolm  
 9 Chang, Steven Chao-Huan  
 11 (ii) TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC  
 12 PROTEINS

14 (iii) NUMBER OF SEQUENCES: 24

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear  
 18 (B) STREET: 620 Newport Center Drive, 16th Floor  
 19 (C) CITY: Newport Beach  
 20 (D) STATE: CA  
 21 (E) COUNTRY: U.S.A.  
 22 (F) ZIP: 92660

**ENTERED**

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Diskette  
 26 (B) COMPUTER: IBM Compatible  
 27 (C) OPERATING SYSTEM: Windows  
 28 (D) SOFTWARE: FastSEQ for Windows Version 2.0b

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/574,819

C--> 32 (B) FILING DATE: 19-May-2000

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 08/836,081

37 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Bartfeld, Neil S  
 41 (B) REGISTRATION NUMBER: 39,901  
 42 (C) REFERENCE/DOCKET NUMBER: NIH099.001APC

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 619-235-8550  
 46 (B) TELEFAX: 619-235-0176  
 47 (C) TELEX:

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 26 base pairs  
 54 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: single  
 56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

59 (ix) FEATURE:

66 (A) NAME/KEY: Other  
 62 (B) LOCATION: 3...21  
 63 (D) OTHER INFORMATION: inosine

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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```

73 GGNTGGMANG AYTGGATHRT NGCNCC
75 (2) INFORMATION FOR SEQ ID NO: 2:
77     (i) SEQUENCE CHARACTERISTICS:
78         (A) LENGTH: 9 amino acids
79         (B) TYPE: amino acid
80         (C) STRANDEDNESS: single
81         (D) TOPOLOGY: linear
83     (ii) MOLECULE TYPE: peptide
84     (ix) FEATURE:
91         (A) NAME/KEY: Other
87         (B) LOCATION: 3...3
88         (D) OTHER INFORMATION: Xaa = Q or N
96     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
W--> 98 Gly Trp Xaa Asp Trp Ile Xaa Ala Pro
99     1           5
101 (2) INFORMATION FOR SEQ ID NO: 3:
103     (i) SEQUENCE CHARACTERISTICS:
104         (A) LENGTH: 26 base pairs
105         (B) TYPE: nucleic acid
106         (C) STRANDEDNESS: single
107         (D) TOPOLOGY: linear
109     (ii) MOLECULE TYPE: cDNA
110     (ix) FEATURE:
112         (A) NAME/KEY: Other
113         (B) LOCATION: 3...24
114         (D) OTHER INFORMATION: inosine
117     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
119 GGNTGGWSNG ARTGGATHAT NWGNCC
121 (2) INFORMATION FOR SEQ ID NO: 4:
123     (i) SEQUENCE CHARACTERISTICS:
124         (A) LENGTH: 9 amino acids
125         (B) TYPE: amino acid
126         (C) STRANDEDNESS: single
127         (D) TOPOLOGY: linear
129     (ii) MOLECULE TYPE: peptide
131     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
133 Gly Trp Ser Glu Trp Ile Ile Ser Pro
134     1           5
136 (2) INFORMATION FOR SEQ ID NO: 5:
138     (i) SEQUENCE CHARACTERISTICS:
139         (A) LENGTH: 23 base pairs
140         (B) TYPE: nucleic acid
141         (C) STRANDEDNESS: single
142         (D) TOPOLOGY: linear
144     (ii) MOLECULE TYPE: cDNA
145     (ix) FEATURE:
147         (A) NAME/KEY: Other
148         (B) LOCATION: 9...9
149         (D) OTHER INFORMATION: A or T or G or C

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152     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
154     ARRGTGTGNA CRATRGCRTG RTT                                     23
156 (2) INFORMATION FOR SEQ ID NO: 6:
158     (i) SEQUENCE CHARACTERISTICS:
159         (A) LENGTH: 8 amino acids
160         (B) TYPE: amino acid
161         (C) STRANDEDNESS: single
162         (D) TOPOLOGY: linear
164     (ii) MOLECULE TYPE: peptide
166     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
168     Asn His Ala Ile Val Gln Thr Leu
169     1           5
171 (2) INFORMATION FOR SEQ ID NO: 7:
173     (i) SEQUENCE CHARACTERISTICS:
174         (A) LENGTH: 23 base pairs
175         (B) TYPE: nucleic acid
176         (C) STRANDEDNESS: single
177         (D) TOPOLOGY: linear
179     (ii) MOLECULE TYPE: cDNA
180     (ix) FEATURE:
182         (A) NAME/KEY: Other
183         (B) LOCATION: 3...18
184         (D) OTHER INFORMATION: inosine
187     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
189     CANSCRCANS HNYBNACNAY CAT                                     23
191 (2) INFORMATION FOR SEQ ID NO: 8:
193     (i) SEQUENCE CHARACTERISTICS:
194         (A) LENGTH: 8 amino acids
195         (B) TYPE: amino acid
196         (C) STRANDEDNESS: single
197         (D) TOPOLOGY: linear
199     (ii) MOLECULE TYPE: peptide
200     (ix) FEATURE:
207         (A) NAME/KEY: Other
203         (B) LOCATION: 2...2
204         (D) OTHER INFORMATION: Xaa = V or I
219     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
W--> 221 Met Xaa Val Xaa Xaa Cys Xaa Cys
222     1           5
224 (2) INFORMATION FOR SEQ ID NO: 9:
226     (i) SEQUENCE CHARACTERISTICS:
227         (A) LENGTH: 4 amino acids
228         (B) TYPE: amino acid
229         (C) STRANDEDNESS: single
230         (D) TOPOLOGY: linear
232     (ii) MOLECULE TYPE: peptide
233     (ix) FEATURE:
240         (A) NAME/KEY: Other
236         (B) LOCATION: 2...2

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237          (D) OTHER INFORMATION: Xaa = any aa
250      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
W--> 252  Arg Xaa Xaa Xaa
253      1
255  (2) INFORMATION FOR SEQ ID NO: 10:
257      (i) SEQUENCE CHARACTERISTICS:
258          (A) LENGTH: 13 amino acids
259          (B) TYPE: amino acid
260          (C) STRANDEDNESS: single
261          (D) TOPOLOGY: linear
263      (ii) MOLECULE TYPE: peptide
265      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
267  Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys
268      1             5             10
270  (2) INFORMATION FOR SEQ ID NO: 11:
272      (i) SEQUENCE CHARACTERISTICS:
273          (A) LENGTH: 2341 base pairs
274          (B) TYPE: nucleic acid
275          (C) STRANDEDNESS: single
276          (D) TOPOLOGY: linear
278      (ii) MOLECULE TYPE: cDNA
280      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
282  TCAAGAACGA GTTATTTTCA GCTGCTGACT GGAGACGGTG CACGTCTGGA TACGAGAGCA      60
283  TTTCCACTAT GGGACTGGAT ACAAACACAC ACCCGGCAGA CTTCAAGAGT TTCAGACTGA      120
284  GGAGAAAACC TTTCCCTTCT GCTGCTACTG CTGCTGCCGC TGCTTTTGAA AGTCCACTTC      180
285  CTTTCATGGT TTTTCCTGCC AAACCAGAGG CACCTTCGCT GCTGCCGCTG TTCTCTTTGG      240
286  TGTCAATCAG CGGCTGGCCA GAGGATGAGA CTCCCCAAAC TCCTCACTTT CTTGCTTTGG      300
287  TACCTGGCTT GGCTGGACCT GGAATTCATC TGCCTGTGT TGGGTGCCCC TGACTTGGGC      360
288  CAGAGACCCC AGGGGTCCAG GCCAGGATTG GCCAAAGCAG AGGCCAAGGA GAGGCCCCCC      420
289  CTGGCCCGGA ACGTCTTCAG GCCAGGGGGT CACAGCTATG GTGGGGGGGC CACCAATGCC      480
290  AATGCCAGGG CAAAGGGAGG CACCGGGCAG ACAGGAGGCC TGACACAGCC CAAGAAGGAT      540
291  GAACCCAAAA AGCTGCCCCC CAGACCGGGC GGCCCTGAAC CCAAGCCAGG ACACCCTCCC      600
292  CAAACAAGGC AGGCTACAGC CCGGACTGTG ACCCAAAAAG GACAGCTTCC CGGAGGCAAG      660
293  GCACCCCAAA AAGCAGGATC TGTCCCCAGC TCCTTCCTGC TGAAGAAGGC CAGGGAGCCC      720
294  GGGCCCCCAC GAGAGCCCAA GGAGCCGTTT CGCCACCCC CCATCACACC CCACGAGTAC      780
295  ATGCTCTCGC TGTACAGGAC GCTGTCCGAT GCTGACAGAA AGGGAGGCAA CAGCAGCGTG      840
296  AAGTTGGAGG CTGGCCTGGC CAACACCATC ACCAGCTTTA TTGACAAAGG GCAAGATGAC      900
297  CGAGGTCCCG TGGTCAGGAA GCAGAGGTAC GTGTTTGACA TTAGTGCCCT GGAGAAGGAT      960
298  GGGCTGCTGG GGGCCGAGCT GCGGATCTTG CGGAAGAAGC CCTCGGACAC GGCCAAGCCA      1020
299  GCGGTCCCCC GGAGCCGGCG GGCTGCCAG CTGAAGCTGT CCAGCTGCCC CAGCGGCCGG      1080
300  CAGCCGGCCG CCTTGCTGGA TGTGCGCTCC GTGCCAGGCC TGGACGGATC TGGCTGGGAG      1140
301  GTGTTTCGACA TCTGGAAGCT CTTCCGAAAC TTAAAGAACT CGGCCAGCT GTGCCTGGAG      1200
302  CTGGAGGCCT GGAACGGGG CAGGACCGTG GACCTCCGTG GCCTGGGCTT CGACCGCGCC      1260
303  GCCCGGCAGG TCCACGAGAA GGCCCTGTTC CTGGTGTTCG GCGCACCAA GAAACGGGAC      1320
304  CTGTTCTTTA ATGAGATTAA GGCCGCTCT GGCCAGGACG ATAAGACCGT GTATGAGTAC      1380
305  CTGTTTCAGC AGCGGCGAAA ACGGCGGGCC CCATCGGCCA CTCGCCAGGG CAAGCGACCC      1440
306  AGCAAGAACC TTAAGGCTCG CTGCAGTCGG AAGGCACTGC ATGTCAACTT CAAGGACATG      1500
307  GGCTGGGACG ACTGGATCAT CGCACCCCTT GAGTACGAGG CTTTCCACTG CGAGGGGCTG      1560
308  TGCGAGTTCC CATTGCGCTC CCACCTGGAG CCCACGAATC ATGCAGTCAT CCAGACCCTG      1620

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309 ATGAACTCGA TGGACCCCGA GTCCACACCA CCCACCTGCT GTGTGCCCAC GCGGCTGAGT 1680
310 CCCATCAGCA TCCTCTTCAT TGA CTCTGCC AACACGTGG TGTATAAGCA GTATGAGGAC 1740
311 ATGGTCGTGG AGTCGTGTGG CTGCAGGTAG CAGCACTGGC CCTCTGTCTT CCTGGGTGGC 1800
312 ACATCCCAAG AGCCCCCTTC TGA CTCTGCC GAATCACAGA GGGGTCAGGA AGCTGTGGCA 1860
313 GGAGCATCTA CACAGCTTGG TGAAGGGATT CAATAAGCTT GCTCGCTCTC TGAGTGTGAC 1920
314 TTGGGCTAAA GGCCCCCTTT TATCCACAAG TTCCCCTGGC TGAGGATTGC TGCCCGTCTG 1980
315 CTGATGTGAC CAGTGGCAGG CACAGGTCCA GGGAGACAGA CTCTGAATGG GACTGAGTCC 2040
316 CAGGAAACAG TGCTTTCCGA TGAGACTCAG CCCACCATTT CTCCTCACCT GGGCCTTCTC 2100
317 AGCCTCTGGA CTCTCCTAAG CACCTCTCAG GAGAGCCACA GGTGCCACTG CCTCCTCAAA 2160
318 TCACATTTGT GCCTGGTGAC TTCCTGTCCC TGGGACAGTT GAGAAGCTGA CTGGGCAAGA 2220
319 GTGGGAGAGA AGAGGAGAGG GCTTGGATAG AGTTGAGGAG TGTGAGGCTG TTAGACTGTT 2280
320 AGATTTAAAT GTATATTGAT GAGATAAAAA GCAAAACTGT GCCTAAAAAA AAAAAAAAAA 2340
321 A 2341
323 (2) INFORMATION FOR SEQ ID NO: 12:
325 (i) SEQUENCE CHARACTERISTICS:
326 (A) LENGTH: 1308 base pairs
327 (B) TYPE: nucleic acid
328 (C) STRANDEDNESS: single
329 (D) TOPOLOGY: linear
331 (ii) MOLECULE TYPE: cDNA
333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
335 CGAGCGTCCG CCGAGCTGGG CTCCGCCAAG GGAATGCGAA CGCGCAAGGA AGGAAGGATG 60
336 CCGCGGGCGC CGAGAGAGAA TGCCACGGCC CGGGAGCCCC TGGATCGCCA GGAGCCCCCG 120
337 CCGAGGCCGC AGGAGGAGCC CCAGCGGCGG CCGCCACAGC AGCCTGAAGC TCGGGAGCCT 180
338 CCCGGCAGGG GCGCGCGCTT GGTGCCCCAC GAGTACATGC TGTCAATCTA CAGGACTTAC 240
339 TCCATCGCCG AGAAGCTGGG CATCAATGCT AGCTTTTTC AGTCTTCAA GTCGGCTAAT 300
340 ACGATCACTA GCTTTGTAGA CAGGGGACTA GACGATCTCT CGCACACTCC TCTCCGGAGA 360
341 CAGAAGTATT TGTTTGATGT GTCCACGCTC TCAGACAAAG AAGAGCTGGT GGGCGCGGAC 420
342 GTGCGGCTGT TTCGCCAGGC GCGCGCTGCC CTGGCGCCGC CGGCGGCCGC TCCGCTTGCA 480
343 GCTCTTCGCC TGCCAGTCGC CCCTGCTGCT GGAAGCGCGG AGCCTGGACC CGCAGGGGCG 540
344 CCGCGCCCCG GCTGGGAAGT CTTGACGCTG TGGCGGGGCC TGCGCCCCCA GCCCTGGAAG 600
345 CAGCTGTGCT TGGAGCTTCG GGCCGCGTGG GCGGCGGAGC CGGGCGCCGC GGAGGACGAG 660
346 GCGCGCACGC CTGGGCCCCA GCAGCCGCCG CCGCGGACC TGCGGAGTCT GGGCTTCGGC 720
347 CGGAGGGTGC GGACCCCCCA GGAGCGCGCC TTGCTCGTCG GTTCTCCAG GTCCAGCGC 780
348 AAGACCTGT TCGCCGAGAT GCGCGAGCAG CTGGGCTCGG CGACCGAGGT GGTGCGCCCC 840
349 GGTGGTGGGG CCGAGGGGTC GGGGCCGCCG CCGCGCCGC CGCCGCCGCC GCGTTCGGG 900
350 ACCCGGACG CTGGGCTCTG GTCGCCCTCG CCTGGCCGCG GCGGCGCAC GGCCTTCGCC 960
351 AGCCGCCACG GCAAGCGGCA CGCAAGAAG TCGAGGCTGC GCTGCAGCAA GAAGCCCCCTG 1020
352 CACGTGAAC TCAAGGAGCT GGGCTGGGAC GACTGGATTA TCGCGCCCCC GGAGTACGAG 1080
353 GCCTACCACT GCGAGGGCGT GTGCGACTTC CCGCTACGCT CGCACCTGGA GCCACCAAC 1140
354 CACGCCATCA TCCAGACGCT GATGAACTCC ATGGACCCCC GCTCCACCCC GCCAGCTGC 1200
355 TCGGTGCCCC CCAAATTGAC TCCCATCAGC ATCTTGTACA TCGACGCGGG CAATAATGTG 1260
356 GTCTACAACG AGTACGAGGA GATGGTGGTG GAGTCGTGCG GCTGCAGG 1308
358 (2) INFORMATION FOR SEQ ID NO: 13:
360 (i) SEQUENCE CHARACTERISTICS:
361 (A) LENGTH: 501 amino acids
362 (B) TYPE: amino acid
363 (C) STRANDEDNESS: single
364 (D) TOPOLOGY: linear

```

**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\09574819.txt

Output Set: N:\CRF3\07312001\I574819.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15